



## RAW SEQUENCE LISTING

DATE: 03/29/2002

PATENT APPLICATION: US/09/896,791B

TIME: 13:35:58

Input Set : A:\EP.txt

Output Set: N:\CRF3\03292002\I896791B.raw

```

4 <110> APPLICANT: Berkenstam, Anders
5      Bertilsson, Gran
6      Poellinger, Lorenz
8 <120> TITLE OF INVENTION: SCREENING METHODS
10 <130> FILE REFERENCE: 13425-040001
12 <140> CURRENT APPLICATION NUMBER: 09/896,791B
13 <141> CURRENT FILING DATE: 2001-06-29
15 <150> PRIOR APPLICATION NUMBER: 60/217,570
16 <151> PRIOR FILING DATE: 2000-07-12
18 <150> PRIOR APPLICATION NUMBER: SE 0002551-0
19 <151> PRIOR FILING DATE: 2000-07-06
21 <160> NUMBER OF SEQ ID NOS: 3
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 460
27 <212> TYPE: DNA
28 <213> ORGANISM: Mus musculus
30 <220> FEATURE:
31 <221> NAME/KEY: misc_feature
32 <222> LOCATION: (1)...(460)
33 <223> OTHER INFORMATION: n = A,T,C or G
35 <400> SEQUENCE: 1
36 gccatggcgt tggggctgca ggcgcgtgagg tcgaacaccg agctgcggaa ggagaagtcg      60
37 cgggaccgcc cgcagccggc gcacgaggag acggaggtgc tgtaccagct ggcgcacact      120
W--> 38 ctgccctttg cgcgcggcgt cacaccntnc tggacaaggc ctccatcatg cgcctcacia      180
W--> 39 tcagctacct gcgcagacc gcctctgcgc acagantgga aaaaggggga gagccactgg      240
40 acgcctgcta cctgaaggcc ctggagggtt tcgtcatggt actcaccgcc gagggagaca      300
41 tggcttacct gtcggaaaat gtcagcaagc acctgggcct cagtcagtgg acctctgttc      360
42 ctccctccctg atacataacc ccactcctgg taccaatttc tctctggagc tcattggaca      420
43 cagtatcttt gattttatca tccctgtgac caagaggaac      460
45 <210> SEQ ID NO: 2
46 <211> LENGTH: 1100
47 <212> TYPE: DNA
48 <213> ORGANISM: Mus musculus
50 <220> FEATURE:
51 <221> NAME/KEY: CDS
52 <222> LOCATION: (19)...(939)
54 <400> SEQUENCE: 2
55 gaattcggca cgagggcc atg gcg ttg ggg ctg cag cgc gtg agg tcg aac      51
56      Met Ala Leu Gly Leu Gln Arg Val Arg Ser Asn
57      1      5      10
59 acc gag ctg cgg aag gag aag tcg cgg gac gcg gcc cgc agc cgg cgc      99
60 Thr Glu Leu Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg

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RECEIVED

61	15	20	25	
63	agc cag gag acg gag gtg ctg tac cag ctg gcg cac act ctg ccc ttt			
64	Ser Gln Glu Thr Glu Val Leu Tyr Gln Leu Ala His Thr Leu Pro Phe			
65	30	35	40	
67	gcg cgc ggc gtc agc gcg cac ctg gac aag gcc tcc atc atg cgc ctc			
68	Ala Arg Gly Val Ser Ala His Leu Asp Lys Ala Ser Ile Met Arg Leu			
69	45	50	55	
71	aca atc agc tac ctg cgc atg cac cgc ctc tgc gca gca ggt gga aaa			243
72	Thr Ile Ser Tyr Leu Arg Met His Arg Leu Cys Ala Ala Gly Gly Lys			
73	60	65	70	75
75	agg ggg aga gcc act gga cgc ctg cta cct gaa ggc cct gga ggg ttt			291
76	Arg Gly Arg Ala Thr Gly Arg Leu Leu Pro Glu Gly Pro Gly Gly Phe			
77	80	85	90	
79	cgt cat ggt act cac cgc cga ggg aga cat ggc tta cct gtc gga aaa			339
80	Arg His Gly Thr His Arg Arg Gly Arg His Gly Leu Pro Val Gly Lys			
81	95	100	105	
83	tgt cag caa gca cct ggg cct cag tca gtg gac ctc tgt tcc tcc tcc			387
84	Cys Gln Gln Ala Pro Gly Pro Gln Ser Val Asp Leu Cys Ser Ser Ser			
85	110	115	120	
87	ctg ata cat aac ccc act cct ggt acc aat ttc tct ctg gag ctc att			435
88	Leu Ile His Asn Pro Thr Pro Gly Thr Asn Phe Ser Leu Glu Leu Ile			
89	125	130	135	
91	gga cac agt atc ttt gat ttt atc cat ccc tgt gac caa gag gaa ctt			483
92	Gly His Ser Ile Phe Asp Phe Ile His Pro Cys Asp Gln Glu Glu Leu			
93	140	145	150	155
95	caa gac gcc ctg acc ccc agg ccg aac ctg tca aag aag aag ctg gaa			531
96	Gln Asp Ala Leu Thr Pro Arg Pro Asn Leu Ser Lys Lys Lys Leu Glu			
97	160	165	170	
99	gcc cca aca gag cgc cac ttt tcc ctg cga atg aag agc acg ctc acc			579
100	Ala Pro Thr Glu Arg His Phe Ser Leu Arg Met Lys Ser Thr Leu Thr			
101	175	180	185	
103	agc aga ggg cgc acg ctc aac ctc aaa gcg gcc acc tgg aag gtg ctg			627
104	Ser Arg Gly Arg Thr Leu Asn Leu Lys Ala Ala Thr Trp Lys Val Leu			
105	190	195	200	
107	cac tgc tca gga cat atg agg gcc tac aag ccc cct gca cag act tcc			675
108	His Cys Ser Gly His Met Arg Ala Tyr Lys Pro Pro Ala Gln Thr Ser			
109	205	210	215	
111	cct gcc ggg agc cct cgc tcc gag cct ccc ctg caa tgc ctg gtg ctt			723
112	Pro Ala Gly Ser Pro Arg Ser Glu Pro Pro Leu Gln Cys Leu Val Leu			
113	220	225	230	235
115	atc tgt gaa gcc atc ccc cag ctc ccc ttc cac gat ggt gct act ctg			771
116	Ile Cys Glu Ala Ile Pro Gln Leu Pro Phe His Asp Gly Ala Thr Leu			
117	240	245	250	
119	ggt ctt cca cag gag aag act ccc atc tct acc tta ttc acc cct ctt			819
120	Gly Leu Pro Gln Glu Lys Thr Pro Ile Ser Thr Leu Phe Thr Pro Leu			
121	255	260	265	
123	tgg aag gca cta ctt tgt ctt gtc aag agg tgg cct gtt cag gtg cta			867
124	Trp Lys Ala Leu Leu Cys Leu Val Lys Arg Trp Pro Val Gln Val Leu			
125	270	275	280	

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127 cag ggg aaa ggg act gaa tcc tct ctc ccc tca tgg gtg ttg tgg gcc      915
128 Gln Gly Lys Gly Thr Glu Ser Ser Leu Pro Ser Trp Val Leu Trp Ala
129      285                      290                      295
131 ctt aac cgg aaa aat tgt cct ggc tag gagggagtga aggacatggc      962
132 Leu Asn Arg Lys Asn Cys Pro Gly
133 300                      305
135 ccagctatcc ttagcccaga aaccacacaaa tgtctccaaa accaccataa agacctctcc      1022
136 ttgttaggca ccagagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1082
137 aaaaaaacat gcggccgc      1100
139 <210> SEQ ID NO: 3
140 <211> LENGTH: 307
141 <212> TYPE: PRT
142 <213> ORGANISM: Mus musculus
144 <400> SEQUENCE: 3
145 Met Ala Leu Gly Leu Gln Arg Val Arg Ser Asn Thr Glu Leu Arg Lys
146 1      5      10      15
147 Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Gln Glu Thr Glu
148      20      25      30
149 Val Leu Tyr Gln Leu Ala His Thr Leu Pro Phe Ala Arg Gly Val Ser
150      35      40      45
151 Ala His Leu Asp Lys Ala Ser Ile Met Arg Leu Thr Ile Ser Tyr Leu
152      50      55      60
153 Arg Met His Arg Leu Cys Ala Ala Gly Gly Lys Arg Gly Arg Ala Thr
154 65      70      75      80
155 Gly Arg Leu Leu Pro Glu Gly Pro Gly Gly Phe Arg His Gly Thr His
156      85      90      95
157 Arg Arg Gly Arg His Gly Leu Pro Val Gly Lys Cys Gln Gln Ala Pro
158      100      105      110
159 Gly Pro Gln Ser Val Asp Leu Cys Ser Ser Ser Leu Ile His Asn Pro
160      115      120      125
161 Thr Pro Gly Thr Asn Phe Ser Leu Glu Leu Ile Gly His Ser Ile Phe
162      130      135      140
163 Asp Phe Ile His Pro Cys Asp Gln Glu Glu Leu Gln Asp Ala Leu Thr
164 145      150      155      160
165 Pro Arg Pro Asn Leu Ser Lys Lys Lys Leu Glu Ala Pro Thr Glu Arg
166      165      170      175
167 His Phe Ser Leu Arg Met Lys Ser Thr Leu Thr Ser Arg Gly Arg Thr
168      180      185      190
169 Leu Asn Leu Lys Ala Ala Thr Trp Lys Val Leu His Cys Ser Gly His
170      195      200      205
171 Met Arg Ala Tyr Lys Pro Pro Ala Gln Thr Ser Pro Ala Gly Ser Pro
172      210      215      220
173 Arg Ser Glu Pro Pro Leu Gln Cys Leu Val Leu Ile Cys Glu Ala Ile
174 225      230      235      240
175 Pro Gln Leu Pro Phe His Asp Gly Ala Thr Leu Gly Leu Pro Gln Glu
176      245      250      255
177 Lys Thr Pro Ile Ser Thr Leu Phe Thr Pro Leu Trp Lys Ala Leu Leu
178      260      265      270
179 Cys Leu Val Lys Arg Trp Pro Val Gln Val Leu Gln Gly Lys Gly Thr

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180		275				280				285									
181	Glu	Ser	Ser	Leu	Pro	Ser	Trp	Val	Leu	Trp	Ala	Leu	Asn	Arg	Lys	Asn			
182		290					295						300						
183	Cys	Pro	Gly																
184	305																		

**VERIFICATION SUMMARY**

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TIME: 13:35:59

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L:38 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:39 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1